



SEQUENCE LISTING

<110> Godfrey, Wayne
Buck, David
Engleman, Edgar G.

<120> Monoclonal Antibodies to a Receptor (ACT-4) on the Surface of Activated CD4+ T-Cells (As Amended)

<130> 16524.010

<140> US 09/852,845

<141> 2001-05-11

<150> US 08/472,940

<151> 1995-06-06

<150> US 08/147,784

<151> 1993-11-03

<160> 2

<210> 1

<211> 1057

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<223> (15)..(845)

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<223> ACT-4-h-1 cDNA

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Met Cys Val Gly Ala Arg Arg Leu Gly Arg Gly Pro	
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tgt gcg gct ctg ctc ctc ctg ggc ctg ggg ctg agc acc gtg acg ggg	98
Cys Ala Ala Leu Leu Leu Leu Gly Leu Gly Leu Ser Thr Val Thr Gly	
15 20 25	
ctc cac tgt gtc ggg gac acc tac ccc agc aac gac cgg tgc tgc cac	146
Leu His Cys Val Gly Asp Thr Tyr Pro Ser Asn Asp Arg Cys Cys His	
30 35 40	
gag tgc agg cca ggc aac ggg atg gtg agc cgc tgc agc cgc tcc cag	194
Glu Cys Arg Pro Gly Asn Gly Met Val Ser Arg Cys Ser Arg Ser Gln	
45 50 55 60	

aac acg gtg tgc cgt ccg tgc ggg ccg ggc ttc tac aac gac gtg gtc	242
Asn Thr Val Cys Arg Pro Cys Gly Pro Gly Phe Tyr Asn Asp Val Val	
65 70 75	
agc tcc aag ccg tgc aag ccc tgc acg tgg tgt aac ctc aga agt ggg	290
Ser Ser Lys Pro Cys Lys Pro Cys Thr Trp Cys Asn Leu Arg Ser Gly	
80 85 90	
agt gag cgg aag cag ctg tgc acg gcc aca cag gac aca gtc tgc cgc	338
Ser Glu Arg Lys Gln Leu Cys Thr Ala Thr Gln Asp Thr Val Cys Arg	
95 100 105	
tgc cgg gcg ggc acc cag ccc ctg gac agc tac aag cct gga gtt gac	386
Cys Arg Ala Gly Thr Gln Pro Leu Asp Ser Tyr Lys Pro Gly Val Asp	
110 115 120	
tgt gcc ccc tgc cct cca ggg cac ttc ttc cca ggc gac aac cag gcc	434
Cys Ala Pro Cys Pro Pro Gly His Phe Ser Pro Gly Asp Asn Gln Ala	
125 130 135 140	
tgc aag ccc tgg acc aac tgc acc ttg gct ggg aag cac acc ctg cag	482
Cys Lys Pro Trp Thr Asn Cys Thr Leu Ala Gly Lys His Thr Leu Gln	
145 150 155	
ccg gcc agc aat agc tcg gac gca atc tgt gag gac agg gac ccc cca	530
Pro Ala Ser Asn Ser Ser Asp Ala Ile Cys Glu Asp Arg Asp Pro Pro	
160 165 170	
gcc acg cag ccc cag gag acc cag ggc ccc ccg gcc agg ccc atc act	578
Ala Thr Gln Pro Gln Glu Thr Gln Gly Pro Pro Ala Arg Pro Ile Thr	
175 180 185	
gtc cag ccc act gaa gcc tgg ccc aga acc tca cag gga ccc tcc acc	626
Val Gln Pro Thr Glu Ala Trp Pro Arg Thr Ser Gln Gly Pro Ser Thr	
190 195 200	
cgg ccc gtg gag gtc ccc ggg ggc cgt gcg gtt gcc gcc atc ctg ggc	674
Arg Pro Val Glu Val Pro Gly Gly Arg Ala Val Ala Ala Ile Leu Gly	
205 210 215 220	
ctg ggc ctg gtg ctg ggg ctg ctg ggc ccc ctg gcc atc ctg ctg gcc	722
Leu Gly Leu Val Leu Gly Leu Leu Gly Pro Leu Ala Ile Leu Leu Ala	
225 230 235	
ctg tac ctg ctc cgg agg gac cag agg ctg ccc ccc gat gcc cac aag	770
Leu Tyr Leu Leu Arg Arg Asp Gln Arg Leu Pro Pro Asp Ala His Lys	
240 245 250	
ccc cct ggg gga ggc agt ttc cgg acc ccc atc caa gag gag cag gcc	818
Pro Pro Gly Gly Gly Ser Phe Arg Thr Pro Ile Gln Glu Glu Gln Ala	
255 260 265	

gac gcc cac tcc acc ctg gcc aag atc tgacctgggc ccaccaaggt 865
 Asp Ala His Ser Thr Leu Ala Lys Ile
 270 275

ggacgctggg ccccgccagg ctggagcccg gagggctctgc tgggcgagca gggcaggtgc 925

aggccgcctg ccccgccacg ctctggggcc aactctgcac cgttctaggt gccgatggct 985

gcctccggct ctctgcttac gtatgccatg catacctcct gccccgcggg accacaataa 1045

aaaccttggc ag 1057

<210> 2

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<212> PRT

<213> Homo sapiens

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<223> deduced amino acid sequence of ACT-4-h-1

<400> 2

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Leu Leu Leu Gly Leu Gly Leu Ser Thr Val Thr Gly Leu His Cys Val
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Gly Asp Thr Tyr Pro Ser Asn Asp Arg Cys Cys His Glu Cys Arg Pro
 35 40 45

Gly Asn Gly Met Val Ser Arg Cys Ser Arg Ser Gln Asn Thr Val Cys
 50 55 60

Arg Pro Cys Gly Pro Gly Phe Tyr Asn Asp Val Val Ser Ser Lys Pro
 65 70 75 80

Cys Lys Pro Cys Thr Trp Cys Asn Leu Arg Ser Gly Ser Glu Arg Lys
 85 90 95

Gln Leu Cys Thr Ala Thr Gln Asp Thr Val Cys Arg Cys Arg Ala Gly
 100 105 110

Thr Gln Pro Leu Asp Ser Tyr Lys Pro Gly Val Asp Cys Ala Pro Cys
 115 120 125

Pro Pro Gly His Phe Ser Pro Gly Asp Asn Gln Ala Cys Lys Pro Trp
 130 135 140

Thr Asn Cys Thr Leu Ala Gly Lys His Thr Leu Gln Pro Ala Ser Asn

145		150		155		160
Ser Ser Asp Ala Ile Cys Glu Asp Arg Asp Pro Pro Ala Thr Gln Pro	165	170	175			
Gln Glu Thr Gln Gly Pro Pro Ala Arg Pro Ile Thr Val Gln Pro Thr	180	185	190			
Glu Ala Trp Pro Arg Thr Ser Gln Gly Pro Ser Thr Arg Pro Val Glu	195	200	205			
Val Pro Gly Gly Arg Ala Val Ala Ala Ile Leu Gly Leu Gly Leu Val	210	215	220			
Leu Gly Leu Leu Gly Pro Leu Ala Ile Leu Leu Ala Leu Tyr Leu Leu	225	230	235	240		
Arg Arg Asp Gln Arg Leu Pro Pro Asp Ala His Lys Pro Pro Gly Gly	245	250	255			
Gly Ser Phe Arg Thr Pro Ile Gln Glu Glu Gln Ala Asp Ala His Ser	260	265	270			
Thr Leu Ala Lys Ile	275					